

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/602,727A

Source:

IFW/6

Date Processed by STIC:

1/18/07

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 01/18/2007

PATENT APPLICATION: US/10/602,727A

TIME: 16:50:19

Input Set : N:\efs\01\_18\_07\10602727a\_efs\PF596P1N\_SeqListing.txt

Output Set: N:\CRF4\01182007\J602727A.raw

4 <110> APPLICANT: Rosen et al.  
 6 <120> TITLE OF INVENTION: Antibodies Against Protective Antigen  
 8 <130> FILE REFERENCE: PF596P1N  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/602,727A  
 C--> 10 <141> CURRENT FILING DATE: 2003-06-25  
 10 <150> PRIOR APPLICATION NUMBER: 60/391,162  
 11 <151> PRIOR FILING DATE: 2002-06-26  
 13 <150> PRIOR APPLICATION NUMBER: 60/406,339  
 14 <151> PRIOR FILING DATE: 2002-08-28  
 16 <150> PRIOR APPLICATION NUMBER: 60/417,305  
 17 <151> PRIOR FILING DATE: 2002-10-10  
 19 <150> PRIOR APPLICATION NUMBER: 60/426,360  
 20 <151> PRIOR FILING DATE: 2002-11-15  
 22 <150> PRIOR APPLICATION NUMBER: 60/434,807  
 23 <151> PRIOR FILING DATE: 2002-12-20  
 25 <150> PRIOR APPLICATION NUMBER: 60/438,004  
 26 <151> PRIOR FILING DATE: 2003-01-06  
 28 <150> PRIOR APPLICATION NUMBER: 60/443,858  
 29 <151> PRIOR FILING DATE: 2003-01-31  
 31 <150> PRIOR APPLICATION NUMBER: 60/443,781  
 32 <151> PRIOR FILING DATE: 2003-01-31  
 34 <150> PRIOR APPLICATION NUMBER: 60/454,613  
 35 <151> PRIOR FILING DATE: 2003-03-17  
 37 <150> PRIOR APPLICATION NUMBER: 60/468,651  
 38 <151> PRIOR FILING DATE: 2003-05-08  
 40 <160> NUMBER OF SEQ ID NOS: 535  
 43 <170> SOFTWARE: PatentIn version 3.4  
 46 <210> SEQ ID NO: 1  
 47 <211> LENGTH: 2295  
 48 <212> TYPE: DNA  
 49 <213> ORGANISM: Bacillus anthracis  
 52 <220> FEATURE:  
 53 <221> NAME/KEY: CDS  
 54 <222> LOCATION: (1)..(2295)  
 56 <400> SEQUENCE: 1  
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 58 Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile  
 59 1 5 10 15  
 61 ctg gtt tct agc acc ggt aac ctg gaa gta atc cag gct gaa gtt aaa 96  
 62 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys  
 63 20 25 30  
 65 cag gaa aac cgt ctg ctc aac gaa tct gag tct tcc tct cag ggc ctg 144  
 66 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu

(p5.6)

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70	Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val			
71	50 55 60			
73	act tct tcc acc acc ggc gac ctg tct att ccg tct tct gaa ctg gag	240		
74	Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu			
75	65 70 75 80			
77	aac atc ccg tct gaa aac cag tac ttc cag tct gct atc tgg tct ggt	288		
78	Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly			
79	85 90 95			
81	ttc att aaa gtt aag aaa tct gac gaa tac acc ttc gct act tct gca	336		
82	Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala			
83	100 105 110			
85	gat aac cac gtt act atg tgg gta gac gac cag gaa gtt atc aac aaa	384		
86	Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys			
87	115 120 125			
89	gct tct aac tct aac aaa atc cgt ctg gaa aaa ggc cgt ctg tac cag	432		
90	Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln			
91	130 135 140			
93	atc aag att caa tac caa cgt gaa aac ccg acc gag aaa ggt ctg gac	480		
94	Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp			
95	145 150 155 160			
97	ttc aaa ctg tac tgg acc gac tct cag aac aag aaa gaa gtt atc tct	528		
98	Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser			
99	165 170 175			
101	tcc gac aac ctg cag ctg ccg gaa ctg aaa cag aaa tct tcc aac tct	576		
102	Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser			
103	180 185 190			
105	cgt aaa aag cgt tct act tct gct ggt ccg acc gtt ccg gac cgt gat	624		
106	Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp			
107	195 200 205			
109	aac gac ggt att ccg gac tct ctg gaa gtt gaa ggc tac acc gta gac	672		
110	Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp			
111	210 215 220			
113	gtt aaa aac aaa cgt acc ttc ctg tct ccg tgg atc tct aac atc cac	720		
114	Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His			
115	225 230 235 240			
117	gaa aag aaa ggt ctg acc aaa tac aaa tct tcc ccg gag aaa tgg tct	768		
118	Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser			
119	245 250 255			
121	acc gct tct gat ccg tac tct gac ttc gaa aaa gtt act ggt cgt atc	816		
122	Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile			
123	260 265 270			
125	gac aaa aac gtt tct ccg gaa gct cgt cac ccg ctg gta gca gcg tac	864		
126	Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr			
127	275 280 285			
129	ccg atc gtt cac gtt gac atg gaa aac att atc ctg tct aaa aac gaa	912		
130	Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu			
131	290 295 300			

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133	gac	cag	tct	acc	cag	aac	acc	gac	tct	caa	act	cgt	acc	atc	tct	aaa	960
134	Asp	Gln	Ser	Thr	Gln	Asn	Thr	Asp	Ser	Gln	Thr	Arg	Thr	Ile	Ser	Lys	
135	305					310				315						320	
137	aac	acc	tct	acc	tct	cgt	act	cac	acc	tct	gaa	gtt	cac	ggg	aac	gct	1008
138	Asn	Thr	Ser	Thr	Ser	Arg	Thr	His	Thr	Ser	Glu	Val	His	Gly	Asn	Ala	
139					325					330					335		
141	gag	gtt	cac	gct	tct	ttc	ttt	gac	atc	ggg	ggc	tct	gta	tct	gct	ggg	1056
142	Glu	Val	His	Ala	Ser	Phe	Phe	Asp	Ile	Gly	Gly	Ser	Val	Ser	Ala	Gly	
143				340					345						350		
145	ttc	tct	aac	tct	aac	tct	tct	acc	gtt	gca	atc	gac	cac	tct	ctg	tct	1104
146	Phe	Ser	Asn	Ser	Asn	Ser	Ser	Thr	Val	Ala	Ile	Asp	His	Ser	Leu	Ser	
147			355					360					365				
149	ctg	gct	ggg	gaa	cgt	acc	tgg	gct	gaa	act	atg	ggc	ctg	aac	acc	gca	1152
150	Leu	Ala	Gly	Glu	Arg	Thr	Trp	Ala	Glu	Thr	Met	Gly	Leu	Asn	Thr	Ala	
151		370					375					380					
153	gac	acc	gct	cgt	ctg	aac	gct	aac	atc	cgt	tac	gtt	aac	acc	ggc	acc	1200
154	Asp	Thr	Ala	Arg	Leu	Asn	Ala	Asn	Ile	Arg	Tyr	Val	Asn	Thr	Gly	Thr	
155	385				390					395					400		
157	gct	ccg	atc	tac	aac	gtt	ctg	ccg	act	acc	tct	ctg	gta	ctg	ggg	aaa	1248
158	Ala	Pro	Ile	Tyr	Asn	Val	Leu	Pro	Thr	Thr	Ser	Leu	Val	Leu	Gly	Lys	
159				405					410						415		
161	aac	cag	acc	ctg	gca	acc	atc	aaa	gct	aag	gaa	aac	cag	ctg	tct	cag	1296
162	Asn	Gln	Thr	Leu	Ala	Thr	Ile	Lys	Ala	Lys	Glu	Asn	Gln	Leu	Ser	Gln	
163				420					425						430		
165	atc	ctg	gct	ccg	aac	aac	tac	tat	ccg	tct	aaa	aac	ctg	gct	ccg	att	1344
166	Ile	Leu	Ala	Pro	Asn	Asn	Tyr	Tyr	Pro	Ser	Lys	Asn	Leu	Ala	Pro	Ile	
167			435					440							445		
169	gca	ctg	aac	gct	cag	gac	gac	ttc	tct	tcc	acc	ccg	atc	act	atg	aac	1392
170	Ala	Leu	Asn	Ala	Gln	Asp	Asp	Phe	Ser	Ser	Thr	Pro	Ile	Thr	Met	Asn	
171		450				455						460					
173	tac	aac	cag	ttc	ctg	gaa	ctg	gag	aaa	acc	aaa	cag	ctg	cgt	ctg	gac	1440
174	Tyr	Asn	Gln	Phe	Leu	Glu	Leu	Glu	Lys	Thr	Lys	Gln	Leu	Arg	Leu	Asp	
175	465				470					475					480		
177	acc	gac	cag	gtt	tac	ggg	aac	atc	gct	acc	tac	aac	ttc	gaa	aac	ggg	1488
178	Thr	Asp	Gln	Val	Tyr	Gly	Asn	Ile	Ala	Thr	Tyr	Asn	Phe	Glu	Asn	Gly	
179				485					490						495		
181	cgt	gtt	cgt	gta	gac	acc	ggc	tct	aac	tgg	tct	gaa	gtt	ctg	ccg	cag	1536
182	Arg	Val	Arg	Val	Asp	Thr	Gly	Ser	Asn	Trp	Ser	Glu	Val	Leu	Pro	Gln	
183				500					505						510		
185	atc	cag	gaa	acc	act	gct	cgt	att	atc	ttc	aac	ggg	aaa	gac	ctg	aac	1584
186	Ile	Gln	Glu	Thr	Thr	Ala	Arg	Ile	Ile	Phe	Asn	Gly	Lys	Asp	Leu	Asn	
187			515						520						525		
189	ctg	gtt	gaa	cgt	cgt	atc	gct	gca	gta	aac	ccg	tct	gac	ccg	ctg	gaa	1632
190	Leu	Val	Glu	Arg	Arg	Ile	Ala	Ala	Val	Asn	Pro	Ser	Asp	Pro	Leu	Glu	
191		530					535					540					
193	acc	act	aaa	ccg	gac	atg	acc	ctg	aaa	gaa	gct	ctg	aaa	atc	gct	ttc	1680
194	Thr	Thr	Lys	Pro	Asp	Met	Thr	Leu	Lys	Glu	Ala	Leu	Lys	Ile	Ala	Phe	
195	545					550					555					560	
197	ggg	ttc	aac	gaa	ccg	aac	ggc	aac	ctg	cag	tac	cag	ggg	aaa	gat	atc	1728

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199          565          570          575
201 acc gaa ttc gac ttt aac ttc gac cag caa acc tct cag aac atc aaa      1776
202 Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys
203          580          585          590
205 aac cag ctg gct gaa ctg aac gct acc aac atc tac acc gtt ctg gac      1824
206 Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
207          595          600          605
209 aaa atc aag ctg aac gct aaa atg aac att ctg atc cgt gat aaa cgt      1872
210 Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
211          610          615          620
213 ttc cac tac gac cgt aac aac atc gct gtt ggt gct gac gaa tct gta      1920
214 Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val
215 625          630          635          640
217 gtt aaa gaa gct cac cgt gag gtt atc aac tct tcc acc gaa ggt ctg      1968
218 Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu
219          645          650          655
221 ctc ctg aac atc gac aaa gat att cgt aaa atc ctg tct ggt tac atc      2016
222 Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile
223          660          665          670
225 gtt gaa atc gaa gac acc gag ggc ctg aaa gaa gtt atc aac gac cgt      2064
226 Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
227          675          680          685
229 tac gat atg ctg aac atc tct tcc ctg cgt cag gac ggt aaa acc ttc      2112
230 Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
231          690          695          700
233 atc gac ttc aaa aag tac aac gat aaa ctg ccg ctg tac atc tct aac      2160
234 Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
235 705          710          715          720
237 ccg aac tac aaa gta aac gtt tac gct gtt acc aaa gaa aac acc att      2208
238 Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
239          725          730          735
241 atc aac ccg tct gaa aac ggt gac acc tct acc aac ggt atc aaa aag      2256
242 Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys
243          740          745          750
245 atc ctg atc ttc tct aag aaa ggc tac gaa atc ggt taa      2295
246 Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
247          755          760
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251 <211> LENGTH: 764
252 <212> TYPE: PRT
253 <213> ORGANISM: Bacillus anthracis
254 <400> SEQUENCE: 2
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258 1          5          10          15
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261          20          25          30
263 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu
264          35          40          45

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266 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val
267      50                      55                      60
269 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu
270 65                      70                      75                      80
272 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly
273                      85                      90                      95
275 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala
276                      100                      105                      110
278 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys
279                      115                      120                      125
281 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln
282      130                      135                      140
284 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp
285 145                      150                      155                      160
287 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser
288                      165                      170                      175
290 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
291                      180                      185                      190
293 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp
294                      195                      200                      205
296 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
297      210                      215                      220
299 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
300 225                      230                      235                      240
302 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser
303                      245                      250                      255
305 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
306                      260                      265                      270
308 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr
309      275                      280                      285
311 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
312      290                      295                      300
314 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys
315 305                      310                      315                      320
317 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala
318                      325                      330                      335
320 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly
321                      340                      345                      350
323 Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser
324      355                      360                      365
326 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
327      370                      375                      380
329 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr
330 385                      390                      395                      400
332 Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
333                      405                      410                      415
335 Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln
336      420                      425                      430
338 Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/602,727A

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Output Set: N:\CRF4\01182007\J602727A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:256; Xaa Pos. 14

**VERIFICATION SUMMARY**

DATE: 01/18/2007

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Input Set : N:\efs\01\_18\_07\10602727a\_efs\PF596PlN\_SeqListing.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:4554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:256 after pos.:0